

## SEQUENCE LISTING

**(1) GENERAL INFORMATION:**

**(i) APPLICANT:**

(A) NAME: Max-Planck-Gesellschaft zur Foerderung der  
Wissenschaften e.V.

(B) STREET: none

(C) CITY: Berlin

(E) COUNTRY: DE

(F) POSTAL CODE (ZIP): none

(ii) **TITLE OF INVENTION:** Nucleic acid molecules encoding an RNA-directed RNA polymerase (RdRP)

(iii) ~~NUMBER OF SEQUENCES: 2.~~

(iv) ~~COMPUTER READABLE FORM:~~

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 3731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Tomato

(ix) **FEATURE:**

(A) NAME/KEY: CDS

(B) LOCATION: 194..3535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAAATATTCT TTA~~CT~~ACTT CACCAGGGAT TGACTCATCA CTCCCTCAA GTCTTTGTGT

120 GTTGTGATAA TAAATTTGGT TGTGCTTCAG TTTCAGTAC TACTGCTGGG TAGTTTTTAT

TTTGATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG  
AACTGCACCT 180

GGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TTC GGA TTC CCT TAT 229  
Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr

**1                  5                  10**

CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA 277  
 Leu Leu Ser Ala Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly  
 15 20 25

TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT 325  
 Tyr Gly Thr Val Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser  
 30 35 40

AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA 373  
 Arg Ala Phe Ala Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys  
 45 50 55 60

ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TTT GGC TCT TCT TAT TTG 421  
 Ile Ile Thr Leu Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu  
 65 70 75

AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG 469  
 Lys Ala Trp Glu Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val  
 80 85 90

GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT 517  
 Asp Gln Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp  
 95 100 105

GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC 565  
 Asp Lys Phe Ala Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly  
 110 115 120

ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC 613  
 Ile Gly Leu Lys Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp  
 125 130 135 140

TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT 661  
 Tyr Lys Leu Gln Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His  
 145 150 155

CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TTT GGT 709  
 Arg Pro Tyr Gly Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly  
 160 165 170

GCT CCT CGG ATC TAT AAG AGA CTT GAA AAC TCC TGT TAT AGC TTC TTT 757  
 Ala Pro Arg Ile Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe  
 175 180 185

AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA 805  
 Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro  
 190 195 200

TCT TGG ATA GGG CTA TCT TCT AGC TTA TGT TTG CAG TTC CGT AGG GGT 853  
 Ser Trp Ile Gly Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly  
 205 210 215 220

GTT CGT CTT CCA AAT TTC GAG GAA AGT TTT TTC CAC TAT GCA GAA CGT 901  
 Val Arg Leu Pro Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg  
 225 230 235

GAA AAC AAT ATT ACT TTA CAG ACT GGT TTC ACC TTT TTC GTC TCT CAA 949  
 Glu Asn Asn Ile Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln

240	245	250	
AAA TCG GCT CTG GTT CCC AAT GTC CAG CCT CCG GAA GGA ATT TCA ATT			997
Lys Ser Ala Leu Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile			
255	260	265	
CCC TAC AAG ATT TTG TTC AAA ATT AGT TCT TTG GTA CAG CAT GGA TGC			1045
Pro Tyr Lys Ile Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys			
270	275	280	
ATA CCT GGG CCA GCA TTA AAT GTC TAC TTT TTC CGA TTA GTT GAT CCT			1093
Ile Pro Gly Pro Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro			
285	290	295	300
CGA AGG AGA AAT GTG GCA TGC ATT GAG CAT GCC TTA GAG AAA CTG TAC			1141
Arg Arg Arg Asn Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr			
305	310	315	
TAT ATA AAG GAG TGC TGT TAT GAT CCC GTG AGG TGG CTC ACT GAG CAG			1189
Tyr Ile Lys Glu Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln			
320	325	330	
TAT GAT GGG TAT CTC AAG GGT AGA CAA CCT CCA AAA TCT CCG TCC ATC			1237
Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile			
335	340	345	
ACT TTA GAT GAT GGG TTG GTG TAT GTA AGA AGG GTC CTA GTA ACA CCA			1285
Thr Leu Asp Asp Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro			
350	355	360	
TGC AAA GTT TAT TTT TGT GGT CCA GAG GTT AAT GTT TCC AAT CGG GTT			1333
Cys Lys Val Tyr Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val			
365	370	375	380
CTC CGC AAT TAT TCT GAA GAC ATA GAT AAC TTT CTT CGT GTT TCT TTT			1381
Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe			
385	390	395	
GTT GAT GAG GAG TGG GAG AAA CTG TAT TCT ACA GAC TTA TTA CCA AAA			1429
Val Asp Glu Glu Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys			
400	405	410	
GCA AGT ACT GGA AGT GGT GTC AGG ACA AAC ATC TAT GAG AGG ATC TTA			1477
Ala Ser Thr Gly Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu			
415	420	425	
TCA ACT CTG CGG AAA GGC TTT GTA ATT GGT GAT AAA AAA TTT GAA TTT			1525
Ser Thr Leu Arg Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe			
430	435	440	
CTT GCA TTT TCA TCG AGC CAG TTG CGG GAT AAT TCA GTG TGG ATG TTT			1573
Leu Ala Phe Ser Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe			
445	450	455	460
GCA TCA AGA CCT GGC CTT ACT GCA AAT GAT ATA AGA GCT TGG ATG GGT			1621
Ala Ser Arg Pro Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly			
465	470	475	

ACA ATG ATG GGA TGT TTG GAT GAA TCC AGA ACC TTG GAA TAT GGT CAG 2341  
Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln

705	710	715	
GTG TTT GTT CAG TTT ACT GGT GCT GGA CAT GGA GAG TTT TCT GAC GAT	2389		
Val Phe Val Gln Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp			
720 725 730			
TTA CAT CCA TTT AAT AAC AGC AGA TCC ACC AAC AGT AAT TTC ATT CTG	2437		
Leu His Pro Phe Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu			
735 740 745			
AAG GGA AAT GTG GTT GTT GCA AAA AAT CCA TGC TTG CAT CCT GGT GAT	2485		
Lys Gly Asn Val Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp			
750 755 760			
ATT CGT GTT TTA AAG GCT GTA AAT GTT CGA GCG CTG CAC CAC ATG GTA	2533		
Ile Arg Val Leu Lys Ala Val Asn Val Arg Ala Leu His His Met Val			
765 770 775 780			
GAT TGT GTT GTA TTC CCT CAG AAA GGA AAA AGA CCT CAT CCG AAT GAA	2581		
Asp Cys Val Val Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu			
785 790 795			
TGT TCT GGG AGT GAT TTG GAT GGG GAT ATC TAC TTT GTT TGC TGG GAT	2629		
Cys Ser Gly Ser Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp			
800 805 810			
CAA GAC ATG ATC CCG CCA AGG CAA GTC CAG CCG ATG GAA TAT CCT CCA	2677		
Gln Asp Met Ile Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro			
815 820 825			
GCA CCC AGC ATA CAG TTG GAC CAT GAT GTC ACA ATT GAG GAA GTT GAA	2725		
Ala Pro Ser Ile Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu			
830 835 840			
GAG TAC TTC ACC AAC TAT ATT GTG AAT GAC AGT TTG GGA ATC ATA GCA	2773		
Glu Tyr Phe Thr Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala			
845 850 855 860			
AAT GCC CAT GTC GTA TTT GCA GAC AGA GAA CCT GAT ATG GCC ATG AGT	2821		
Asn Ala His Val Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser			
865 870 875			
GAT CCA TGC AAA AAA CTT GCT GAG CTC TTT TCA ATT GCA GTG GAC TTT	2869		
Asp Pro Cys Lys Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe			
880 885 890			
CCA AAG ACT GGT GTT CCC GCT GAA ATA CCA TCT CAG TTG CGC CCT AAA	2917		
Pro Lys Thr Gly Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys			
895 900 905			
GAA TAC CCA GAC TTC ATG GAT AAG CCG GAC AAG ACC AGC TAT ATC TCA	2965		
Glu Tyr Pro Asp Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser			
910 915 920			
GAA AGA GTT ATT GGA AAG CTT TTC AGG AAA GTG AAG GAC AAA GCA CCT	3013		
Glu Arg Val Ile Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro			
925 930 935 940			

CAG GCT AGC TCT ATC GCG ACC TTC ACA AGA GAT GTT GCA AGG AGA TCA 3061  
 Gln Ala Ser Ser Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser  
 945 950 955

TAT GAT GCT GAT ATG GAA GTT GAT GGA TTT GAA GAT TAC ATT GAC GAA 3109  
 Tyr Asp Ala Asp Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu  
 960 965 970

GCT TTT GAC TAC AAA ACT GAA TAT GAC AAC AAG CTG GGT AAT TTA ATG 3157  
 Ala Phe Asp Tyr Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met  
 975 980 985

GAC TAC TAT GGC ATA AAA ACA GAG GCT GAA ATA CTT AGT GGT GGC ATT 3205  
 Asp Tyr Tyr Gly Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile  
 990 995 1000

ATG AAG GCA TCA AAA ACT TTT GAC CGC AGA AAA GAT GCT GAG GCC ATT 3253  
 Met Lys Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile  
 1005 1010 1015 1020

AGT GTT GCT GTG AGG GCC TTG AGG AAG GAG GCA AGA GCC TGG TTC AAG 3301  
 Ser Val Ala Val Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys  
 1025 1030 1035

AGG CGT AAT GAT ATA GAT GAC ATG TTA CCA AAG GCT TCG GCT TGG TAC 3349  
 Arg Arg Asn Asp Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr  
 1040 1045 1050

CAC GTT ACA TAT CAT CCT ACA TAT TGG GGT TGC TAC AAT CAG GGG TTG 3397  
 His Val Thr Tyr His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu  
 1055 1060 1065

AAA AGA GCT CAT TTC ATT AGC TTT CCC TGG TGT GTT TAT GAC CAG CTA 3445  
 Lys Arg Ala His Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu  
 1070 1075 1080

ATC CAG ATT AAG AAG GAC AAA GCA CGT AAC AGG CCA GTT CTC AAC TTG 3493  
 Ile Gln Ile Lys Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu  
 1085 1090 1095 1100

TCA TCT CTC AGG GCT CAA CTG AGT CAC AGA TTA GTG TTG AAA 3535  
 Ser Ser Leu Arg Ala Gln Leu Ser His Arg Leu Val Leu Lys  
 1105 1110

TGAGATTCCA GTCGAGCGTT AAGCTGATAT ATATATAATG TAATAGGGTG  
 TGATCATAAG 3595

AAAACTGTTA TGCATTGTTG ACTACCTTTT GTCTTTAAAA CTGCATGAAG CTGCAACATA  
 3655

TATGCAGTAC TCTAAGAAAC AGATGTACAG CTAAGTACTA ATATGTATGT  
 GATTTGAGTT 3715

TCATCTTTCT TCTAAA 3731

(2) INFORMATION FOR SEQ ID NO: 2:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 2:

Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile Pro Tyr Lys Ile  
260 265 270

Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys Ile Pro Gly Pro  
275 280 285

Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro Arg Arg Arg Asn  
290 295 300

Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr Tyr Ile Lys Glu  
305 310 315 320

Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln Tyr Asp Gly Tyr  
325 330 335

Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile Thr Leu Asp Asp  
340 345 350

Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro Cys Lys Val Tyr  
355 360 365

Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val Leu Arg Asn Tyr  
370 375 380

Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe Val Asp Glu Glu  
385 390 395 400

Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys Ala Ser Thr Gly  
405 410 415

Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu Ser Thr Leu Arg  
420 425 430

Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe Leu Ala Phe Ser  
435 440 445

Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe Ala Ser Arg Pro  
450 455 460

Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly Asp Phe Ser Gln  
465 470 475 480

Ile Lys Asn Val Ala Lys Tyr Ala Ala Arg Leu Gly Gln Ser Phe Gly  
485 490 495

Ser Ser Arg Glu Thr Leu Ser Val Leu Arg His Glu Ile Glu Val Ile  
500 505 510

Pro Asp Val Lys Val His Gly Thr Ser Tyr Val Phe Ser Asp Gly Ile  
515 520 525

Gly Lys Ile Ser Gly Asp Phe Ala His Arg Val Ala Ser Lys Cys Gly  
530 535 540

Leu Gln Tyr Thr Pro Ser Ala Phe Gln Ile Arg Tyr Gly Gly Tyr Lys  
545 550 555 560

Gly Val Val Gly Val Asp Pro Asp Ser Ser Met Lys Leu Ser Leu Arg  
565 570 575

00763374-023303



Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe Pro Lys Thr Gly

895

Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser Glu Arg Val Ile  
915 920 925

Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro Gln Ala Ser Ser  
930 935 940

~~Ile~~ Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser Tyr Asp Ala Asp  
 945                      950                      955                      960

Met Glu Val Asp Gly Phe Gln Asp Tyr Ile Asp Glu Ala Phe Asp Tyr  
965 970 975

Lys Thr Glu Tyr Asp ~~Asn~~ Lys Leu Gly Asn Leu Met Asp Tyr Tyr Gly  
980 985 990

Ile Lys Thr Glu Ala ~~Glu Ile~~ ~~Leu~~ Ser Gly Gly Ile Met Lys Ala Ser  
 995                      1000                      1005

Lys Thr Phe Asp Arg Arg Lys Asp ~~Ala~~ Glu Ala Ile Ser Val Ala Val  
1010 1015 1020

Arg Ala Leu Arg Lys Gln Ala Arg Ala Thr Phe Lys Arg Arg Asn Asp  
1025                    1030                    1035                    1040

Ile Asp Asp Met Leu Pro Lys Ala Ser Ala ~~Tyr Tyr~~ His Val Thr Tyr  
1045 1050 1055

His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly ~~Leu~~ Lys Arg Ala His  
1060 1065 1070

Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu Ile Gln Ile Lys  
1075 1080 1085

Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu Ser Ser Leu Arg  
1090 1095 1100

Ala Gln Leu Ser His Arg Leu Val Leu Lys  
1105                    1110